Amendments

In the Claims:

Please cancel claims 1-8 and 21-23 (claims 9-20 were previously canceled). Please add claims 24-48.

1.-23. (Canceled)

24. (New) A method for creating a model for classifying a biological sample as being of a first state or a second state different than the first state, comprising:

determining the location of a first set of vectors and a second set of vectors in a vector space, each vector of the first set of vectors being obtained from a data stream derived from a biological sample known to be of the first state, the second set of vectors including a plurality of vectors, each of the plurality of vectors of the second set of vectors being associated with a data stream derived from a biological sample known to be of the second state; and

identifying a cluster disposed within the vector space, the cluster containing at least one of the vectors of the first set of vectors, the cluster being associated with the first state for purposes of classifying a biological sample.

25. (New) The method of claim 24, the cluster being a first cluster, further comprising:

identifying a second cluster disposed within the vector space, the second cluster containing at least one of the vectors of the second set of vectors that is associated with a data stream derived from a biological sample known to be of the second state.

26. (New) The method of claim 25, wherein the first cluster and the second cluster do not overlap within the vector space.

27. (New) The method of claim 25, wherein the first cluster is devoid of vectors of the second set of vectors, the second cluster is devoid of vectors of the first set of vectors.

28. (New) The method of claim 24, wherein the data stream derived from the biological sample known to be of the first state is derived via a high throughput bio-assay technique.

29. (New) The method of claim 24, wherein the cluster includes a centroid and a decision hyper-radius.

30. (New) The method of claim 24, further comprising:

abstracting the data stream derived from the biological sample known to be of the first state to obtain a vector that is associated with the data stream.

31. (New) A method for creating a cluster map by which biological samples can be classified into one of a first state and a second state, comprising:

processing a plurality of data strings against a predefined set of variables, thereby creating one or more processed strings, each data string being derived from a biological sample known to be of the first state or the second state;

creating a best lead cluster map for the processed strings, wherein the best lead cluster map includes one or more clusters;

determining a cluster homogeneity for the best lead cluster map;

determining whether the homogeneity of the best lead cluster map is within an acceptable tolerance; and

if it is determined that the homogeneity of the best lead cluster map is within the acceptable tolerance, providing the best lead cluster map.

32. (New) The method of claim 31, the predefined set of variables being a first set of variables, further comprising:

if it is determined that the homogeneity of the best lead cluster map is not within the acceptable tolerance, defining a second set of variables different than the first set of variables.

33. (New) The method of claim 32, further comprising:

processing the plurality of data strings against the second set of variables; and

repeating the creating, determining a cluster, determining whether the homogeneity, and providing.

34. (New) The method of claim 32, wherein the second set of variables are determined using a genetic algorithm.

35. (New) The method of claim 31, wherein the acceptable tolerance is input by a user.

36. (New) The method of claim 31, wherein the predefined set of chromosome variables are input by a user.

37. (New) The method of claim 31, wherein the data strings are derived from a biological sample via a high throughput bio-assay technique.

38. (New) The method of claim 31, wherein each of the clusters includes a centroid and a decision hyper-radius.

39. (New) A method of constructing a model configured to classify biological samples as being of one of at least a first state and a second state different than the first state, comprising:

providing a plurality of data streams, each data stream being derived from a biological sample known to be of the first state or the second state;

selecting a logical chromosome that specifies the location of data in each of the plurality of data streams;

calculating a biological sample vector for each member of the set of data steams using the logical chromosome;

finding the locations in a vector space of at least two non-overlapping data clusters that best fit the sample vectors;

determining a cluster homogeneity for at least one of the at least two non-overlapping data clusters;

determining whether the homogeneity of the at least one of the at least two non-overlapping data clusters is within an acceptable tolerance; and

if it is determined that the homogeneity of at least one of the at least two non-overlapping data clusters is within the acceptable tolerance, providing the locations in the vector space of the at least two non-overlapping data clusters.

40. (New) The method of claim 39, the logical chromosome being a first logical chromosome, further comprising:

if it is determined that the homogeneity of the at least two non-overlapping data clusters is not within the acceptable tolerance, defining a second logical chromosome different than the first logical chromosome.

41. (New) The method of claim 40, wherein the second logical chromosome is defined by using a genetic algorithm.

42. (New) The method of claim 40, further comprising:

calculating a biological sample vector for each member of the set of data steams using the second logical chromosome; and

repeating the finding step.

43. (New) The method of claim 39, wherein the number of preclassified biological samples is greater than 20.

44. (New) The method of claim 39, wherein the number of preclassified biological samples is between 20 and 200.

45. (New) The method of claim 39, wherein the vector space has greater than 3 dimensions.

46. (New) The method of claim 39, wherein the vector space has between 5 and 25 dimensions.

47. (New) The method of claim 39, wherein the logical chromosome is randomly selected.

48. (New) The method of claim 39, wherein the location of each data cluster is the centroid of the sampled vectors that rest in the data cluster.